



Seq List 10-644355.txt

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Mc Wherter, Charles  
Feng, Yiqing  
Mc Kearn, John  
Staten, Nicholas  
Streeter, Philip  
Woulfe, Susan  
Minster, Nancy  
Minnerly, John
- (ii) TITLE OF THE INVENTION: Circular Permuteins of FLT3 Ligand
- (iii) NUMBER OF SEQUENCES: 151
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Carol M. Nielsen, Gardere Wynne Sewell LLP
  - (B) STREET: 1000 Louisiana, Suite 3400
  - (C) CITY: Houston
  - (D) STATE: Texas
  - (E) COUNTRY: USA
  - (F) ZIP: 77002
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: CD
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Unknown
  - (B) FILING DATE: 20-AUG-2003
  - (C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/955,090
  - (B) FILING DATE: 21-OCT-97
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/030,094
  - (B) FILING DATE: 25-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Nielsen, Carol M.
  - (B) REGISTRATION NUMBER: 37,676
  - (C) REFERENCE/DOCKET NUMBER: 126181-1059
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 713-276-5383
  - (B) TELEFAX: 713-276-5555
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 amino acids

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(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Ala	Leu
		35					40					45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50				55						60				
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65				70					75						80
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Gln	Glu	Thr	Ser	Glu	Gln	
		100					105					110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115				120						125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro									
	130					135									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35					40					45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50				55						60				
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65				70					75						80
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Gln	Glu	Thr	Ser	Glu	Gln	
		100					105					110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115				120						125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe
 1      5      10      15
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro
 20      25      30
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu
 35      40      45
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val
 50      55      60
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile
 65      70      75      80
His Phe Val Thr Lys Cys Ala Phe Gln Glu Thr Ser Glu Gln Leu Val
 85      90      95
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu
 100      105      110
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
 115      120

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe
 1      5      10      15
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro
 20      25      30
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu
 35      40      45
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val
 50      55      60
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile
 65      70      75      80
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg
 85      90      95
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln
 100      105      110
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys
 115      120      125
Leu Glu Leu Gln Cys Gln Pro
 130      135

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35				40						45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50				55					60					
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70				75					80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90				95		
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
		100				105						110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115				120						125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35				40						45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50				55					60					
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70				75					80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90				95		
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
		100				105						110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115				120						125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro									
	130					135									

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35					40					45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55					60				
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70				75					80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85				90					95		
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Gln	Glu	Thr	Ser	Glu	Gln	
			100				105					110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115				120					125				
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5					10					15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35					40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55				60					
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70				75					80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
				85				90					95		
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly	Asn	Gly	Ser
			100				105						110		
Gly	Gly	Asn	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
		115				120						125			
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
	130					135					140				
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1      5      10      15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 20      25      30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 35      40      45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50      55      60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 65      70      75      80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 85      90      95
Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr
100      105      110
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val
115      120      125
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr
130      135      140
Val Ala Ser Asn Leu Gln
145      150

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1      5      10      15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 20      25      30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 35      40      45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50      55      60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 65      70      75      80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 85      90      95
Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe
100      105      110
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
115      120      125
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
130      135      140
Gln
145

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
 1      5      10
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe
      20      25      30
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
      35      40      45
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
      50      55      60
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly
65      70      75      80
Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe
      85      90      95
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
      100      105      110
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
      115      120      125
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
130      135      140
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
 1      5      10
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
      20      25      30
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
      35      40      45
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
      50      55      60
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly
65      70      75      80
Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile
      85      90      95
Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu
      100      105      110
Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
      115      120      125
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
130      135      140
Leu Lys Thr Val Ala Gly
145      150

```

(2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
 1      5      10      15
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
 20      25      30
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
 35      40      45
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
 50      55      60
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly
 65      70      75      80
Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala
 85      90      95
Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
100      105      110
Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp
115      120      125
Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala
130      135      140
Gly
145

```

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
 1      5      10      15
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
 20      25      30
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
 35      40      45
Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser Gly Gly
 50      55      60
Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
 65      70      75      80
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
 85      90      95
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
100      105      110
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
115      120      125
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
130      135      140
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro
145      150      155

```



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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
 1          5          10          15
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
          20          25          30
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
          35          40          45
ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr Gln Asp
          50          55          60
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile
          65          70          75          80
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala
          85          90          95
ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val
          100          105          110
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys
          115          120          125
Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr
          130          135          140
Lys Cys Ala Phe Gln Pro
          145          150

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
 1          5          10          15
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
          20          25          30
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
          35          40          45
Ser Thr Leu Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His
          50          55          60
Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp
          65          70          75          80
Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp
          85          90          95
Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp
          100          105          110
Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu
          115          120          125
Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln
          130          135          140          145

```

130

135

140

Pro  
145

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5					10					15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35					40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70				75					80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
			85					90					95		
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Ser	Gly	Ser
			100					105					110		
Gly	Gly	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
		115					120					125			
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
	130					135					140				
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
145					150					155					

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5					10					15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35					40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70				75					80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
			85					90					95		
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Ser	Gly	Thr
			100					105					110		

## Seq List 10-644355.txt

Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val  
 115 120 125  
 Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr  
 130 135 140  
 Val Ala Ser Asn Leu Gln  
 145 150

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp  
 1 5 10 15  
 Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
 20 25 30  
 Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly  
 35 40 45  
 Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr  
 50 55 60  
 Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu  
 65 70 75 80  
 Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu  
 85 90 95  
 Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu  
 100 105 110  
 Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg  
 115 120 125  
 Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly  
 130 135 140  
 Ser  
 145

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser  
 1 5 10 15  
 Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln  
 20 25 30  
 Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys  
 35 40 45  
 Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu  
 50 55 60  
 Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn  
 65 70 75 80  
 Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser

## Seq List 10-644355.txt

```

      85      90      95
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr
      100      105      110
ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe
      115      120      125
ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
      130      135      140

```

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
 1      5      10      15
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
      20      25      30
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
      35      40      45
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
      50      55      60
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
65      70      75      80
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
      85      90      95
Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
      100      105      110
Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
      115      120      125
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly
      130      135      140
ser Gly Gly Gly Ser
145

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Gly Ser Gly Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile
 1      5      10      15
Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu
      20      25      30
Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
      35      40      45
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
      50      55      60
Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val
65      70      75      80

```

Seq List 10-644355.txt

```

Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro
      85      90
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu
      100      105      110
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn
      115      120      125
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
      130      135      140

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Met Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
 1      5      10      15
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
      20      25      30
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
      35      40      45
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
      50      55      60
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
      65      70      75      80
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
      85      90      95
Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
      100      105      110
Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
      115      120      125
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly
      130      135      140
Ser Gly Gly Gly Ser Gly Gly Gly Ser
      145      150

```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Cys Ser
 1      5      10      15
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu
      20      25      30
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
      35      40      45
Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala
      50      55      60
Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln

```

## Seq List 10-644355.txt

```

65      70      75      80
Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys
      85      90      95
Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile
      100      105      110
Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro
      115      120      125
Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln
      130      135      140
Pro Asp Ser Ser Thr Leu
145      150

```

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1      5      10      15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
      20      25      30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
      35      40      45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
      50      55      60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
      65      70      75      80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
      85      90      95
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser
      100      105      110
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu
      115      120      125
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
      130      135      140
Leu Gln
145

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1      5      10      15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
      20      25      30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
      35      40      45

```

Seq List 10-644355.txt

```

Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50      55      60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
65      70      75      80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
      85      90      95
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Thr Gln Asp Cys
      100      105      110
Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg
      115      120      125
Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser
130      135      140
Asn Leu Gln
145

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1      5      10      15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
      20      25      30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
      35      40      45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50      55      60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
65      70      75      80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
      85      90      95
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Thr
      100      105      110
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val
      115      120      125
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr
130      135      140
Val Ala Ser Asn Leu Gln
145      150

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1      5      10      15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly

```

Seq List 10-644355.txt

Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35					40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75					80
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
			85						90					95	
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
			100					105					110		
Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
		115					120					125			
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
	130					135					140				
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln							
145					150										

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10					15		
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
		20						25				30			
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35					40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75					80
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
			85					90					95		
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
			100					105					110		
Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
		115					120					125			
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
	130				135						140				
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
145					150				155						

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:



## Seq List 10-644355.txt

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1      5      10      15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 20      25      30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 35      40      45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50      55      60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 65      70      75      80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 85      90      95
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
100      105      110
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe
115      120      125
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
130      135      140
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
145      150      155      160
Gln

```

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Ala Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
 1      5      10      15
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
 20      25      30
Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val
 35      40      45
Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro
 50      55      60
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu
 65      70      75      80
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn
 85      90      95
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
100      105      110
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr
115      120      125
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val
130      135      140
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
145      150      155

```

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## Seq List 10-644355.txt

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Ala Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg
 1      5      10      15
Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly
 20      25      30
Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe
 35      40      45
Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val
 50      55      60
Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val
 65      70      75
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu
 85      90      95
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly
100      105      110
Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr Gln Asp Cys Ser Phe Gln
115      120      125
His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser
130      135      140
Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Ala Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
 1      5      10      15
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
 20      25      30
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
 35      40      45
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
 50      55      60
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly
 65      70      75
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr Gln Asp
 85      90      95
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile
100      105      110
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala
115      120      125
Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val
130      135      140
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

## Seq List 10-644355.txt

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His
1				5					10					15	
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe
			20					25					30		
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu
		35					40					45			
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu
	50					55					60				
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly
65					70					75					80
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe
			85					90						95	
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
			100					105					110		
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
		115					120					125			
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
	130					135					140				
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu
1				5					10					15	
Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr
			20					25					30		
Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser
		35					40					45			
Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly
	50					55					60				
Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
65				70					75						80
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
			85						90					95	
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly
			100					105					110		
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr
		115					120					125			
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu
	130					135					140				
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:36:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Ala Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
 1      5      10      15
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
 20      25      30
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly
 35      40      45
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr Gln Asp
 50      55      60
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile
 65      70      75      80
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala
 85      90      95
Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val
100      105      110
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys
115      120      125
Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr
130      135      140
Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Ala Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val
 1      5      10      15
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu
 20      25      30
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly
 35      40      45
Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr Gln Asp Cys Ser Phe Gln
 50      55      60
His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser
 65      70      75      80
Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
 85      90      95
Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg
100      105      110
Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu
115      120      125
Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe
130      135      140
Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln
145      150      155

```

145

150

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Ser  
1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Gly Gly Ser Gly Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Gly Gly Ser Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Phe Gly Asn Met  
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Phe Gly Gly Asn Met  
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Phe Gly Gly Asn Gly Gly Asn Met  
1 5

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Ser Asp Met Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser Gly Gly Asn Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Gly Gly Ser Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Gly Gly Ser Gly Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
 1 5 10 15  
 Gly Gly Gly Ser Gly  
 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGACCATGG CNACCCAGGA CTGCTCCTTC CAA

33

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACTGAAGCTT AGGGCTGACA CTGCAGCTCC AG

32

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTGAAGCTT ACAGGGTTGA GGAGTCGGGC TG

32

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC

46

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC

46

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TGTCCAAACT CATCAATGTA TC

22

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

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CATGGCCATG GCCGACGAGG AGCTCTGCGG GGGCCTCT 38

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTAGAAGCT TACTGCAGGT TGGAGGCCAC GGTGAC 36

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CATGGCCATG GCCTCCAAGA TGCAAGGCTT GCTGGAGC 38

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCTAGAAGCT TACCCAGCGA CAGTCTTGAG CCGCTC 36

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CATGGCCATG GCCCCCCCCA GCTGTCTTCG CTTCGT 36

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTAGAAGCT TAGGGCTGAA AGGCACATTT GGTGACA

37

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CCCTGTCTGG CGGCAACGGC ACCCAGGACT GCTCCTTCCA AC

42

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCGGTAACGG CAGTGGAGGT AATGGCACCC AGGACTGCTC CTTCCAAC

48

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACGGCAGTGG TGGCAATGGG AGCGGCGGAA ATGGAACCCA GGACTGCTCC TTCCAAC

57

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTGCCGTTGC CGCCAGACAG GGTGAGGAG TCGGGCTG

38

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTACCTCCA CTGCCGTTAC CGCCTGACAG GGTGAGGAG TCGGGCTG 48

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCTCCCATTG CCACCACTGC CGTTACCTCC AGACAGGGTT GAGGAGTCGG GCTG 54

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GATGAGGATC CGGTGGCAAT GGGAGCGGCG GAAATGGAAC CCAGGACTGC TCCTTCCACC 60

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GATGACGGAT CCGTTACCTC CAGACAGGGT TGAGGAGTCG GGCTG 45

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATGACGGAT CCGGAGGTAA TGGCACCCAG GACTGCTCCT TCCAAC 46

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GACTGCCATG GCCGACGAGG AGCTCTGCG

29

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GACTCAAGCT TACTGCAGGT TGGAGGCC

28

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GACTCGGGAT CCGGAGGTTC TGGCACCCAG GACTGCTCC

39

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GACTGGGATC CGGTGGCAGT GGGAGCGGCG GATCTGGAAC C

41

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GACTTGGGAT CCACTACCTC CAGACAGGGT TGAGGAGTC

39

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACTGACGGAT CCACCGCCCA GGGTTGAGGA GTCGGGCTG

39

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACTGACGGAT CCACCTCCTG ACCCACC GCC CAGGGTTGAG GAGTCGGGCT G

51

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ACTGACGGAT CCACCTCCTG ACCCACCCTCC TGACCCACCG CCCAGGGTTG AGGAGTCGGG  
CTG

60  
63

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACGTAAAGCT TACAGGGTTG AGGAGTCG

28

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCAGTGGAT CCGGAGGTAC CCAGGACTGC TCCTTCCAAC

40

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCAGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AAC

43

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTCAGTGGAT CCGGAGGTGG CTCAGGGGGA GGTAGTGGTA CCCAGGACTG CTCCTTCCAC

60

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTTGCCATGG CNTCNAAYCT GCARGAYGAR GARCTGTGCG GGGGCCTCTG GCGGCTG

57

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTTGCCATGG CNAAYCTGCA RGAYGARGAR CTGTGYGGGG GCCTCTGGCG GCTGGTC

57

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:



GTTGCCATGG CNCTGCARGA YGARGARCTG TGYGGYGGCC TCTGGCGGCT GGTCCTG 57

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GTTGCCATGG CNCARGAYGA RGARCTGTGY GGYGGYCTCT GGCGGCTGGT CCTGGCA 57

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTTGCCATGG CNGAYGARGA RCTGTGYGGY GGYCTCTGGC GGCTGGTCCT GGCACAG 57

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTGCCATGG CNGARGARCT GTGYGGYGGY CTCTGGCGGC TGGTCCTGGC ACAGCGC 57

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGCCATGG CNGARCTGTG YGGYGGYCTG TGGCGYCTGG TCCTGGCACA GCGCTGG 57

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTGCCATGG CNCTGTGYGG YGGYCTGTGG CGYCTGGTCC TGGCACAGCG CTGGATG

57

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAAGCT TAGGCCACGG TGA CTGGGTA

30

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TATGCAAGCT TAGGAGGCCA CGGTGACTGG

30

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGCAAGCT TAGTTGGAGG CCACGGTGAC

30

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TATGCAAGCT TACAGGTTGG AGGCCACGGT

30

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TATGCAAGCT TACTGCAGGT TGGAGGCCAC 30

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TATGCAAGCT TAGTCCTGCA GGTGGAGGC 30

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TATGCAAGCT TACTCGTCCT GCAGGTTGGA 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TATGCAAGCT TACTCCTCGT CCTGCAGGT 30

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGC	GCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

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(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCCGACTC	CTCAACCCTG	420

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGGAG	ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	300
TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	CTGGAGCTGC	AGTGTGAGCC	CGACTCCTCA	360
ACCCTG						366

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGAACTCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGTACCCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCCGACTC	CTCAACCCTG	420

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCACTCAGG	ACTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCACTCAGG	ACTGCTCTTT	TCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCCGACTC	CTCAACCCTG	420

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

## Seq List 10-644355.txt

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAACGGATC	CGGTGGCAAT	GGGAGCGGCG	GAAATGGAAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAACGGCAG	TGGAGGTAAT	GGCAGCCAGG	ACTGCTCCTT	CCAACACAGC	360
CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	420
TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG				450

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGCG	GCAACGGCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	360
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	420
GCCTCCAACC	TGCAG					435

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180

## Seq List 10-644355.txt

TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	AGGTAACGGA	240
TCCGGTGGCA	ATGGGAGCGG	CGGAAATGGA	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTCTG	CTGGG		465

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	AGGTAACGGA	240
TCCGGAGGTA	ATGGCACCCA	GGACTGCTCC	TTCCAACACA	GCCCCATCTC	CTCCGACTTC	300
GCTGTCAAAA	TCCGTGAGCT	GTCTGACTAC	GTGCTTCAAG	ATTACCCAGT	CACCGTGGCC	360
TCCAACCTGC	AGGACGAGGA	GCTCTGCGGG	GGCCTCTGGC	GGCTGGTCCT	GGCACAGCGC	420
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG				450

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	CGGCAACGGC	240
ACGCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	300
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	360
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	420
AAGACTGTCTG	CTGGG					435

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCTGGAG	GTAACGGCAG	TGGTGGCAAT	180
GGGAGCGGTG	GAAATGGAAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	360

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CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC	420
GTGAACACGG AGATACACTT TGTCACCAA TGTGCCTTTC AGCCC	465

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCAAGCG	GTAACGGCAG	TGGAGGTAAT	180
GGCAGCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	240
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	300
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	360
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	420
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC				450

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCTGGCG	GCAACGGCAC	GCAGGACTGC	180
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	240
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	300
GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	AGCGGCTCAA	GACTGTCGCT	360
GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAA	420
TGTGCCTTTC	AGCCC					435

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTGCCT	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAGTGGATC	CGGAGGTTCT	GGCAACCCAG	GACTGCTCCT	TCCAACACAG	360
CCCCATCTCC	TCCGACTTCG	CTGTCAAAAT	CCGTGAGCTG	TCTGACTACC	TGCTTCAAGA	420
TTACCCAGTC	ACCGTGGCCT	CCAACCTGCA	G			451



## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAAGTGGATC	CGGTGGCAGT	GGGAGCGGCG	GATCTGGAAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGATCC					437

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GGATCCGGAG	GTACCCAGGA	CTGCTCCTTC	CAACACAGCC	CCATCTCCTC	CGACTTCGCT	60
GTCAAAATCC	GTGAGCTGTC	TGACTACCTG	CTTCAAGATT	ACCCAGTCAC	CGTGGCCTCC	120
AACCTGCAGG	ACGAGGAGCT	CTGCGGGGGC	CTCTGGCGGC	TGGTCTTGGC	ACAGCGCTGG	180
ATGGAGCGGC	TCAAGACTGT	CGCTGGGTCC	AAGATGCAAG	GCTTGCTGGA	GCGCGTGAAC	240
ACGGAGATAC	ACTTTGTAC	CAAATGTGCC	TTTCAGCCCC	CCCCCAGCTG	TCTTCGCTTC	300
GTCCAGACCA	ACATCTCCCG	CCTCCTGCAG	GAGACCTCCG	AGCAGCTGGT	GGCGCTGAAG	360
CCCTGGATCA	CTCGCCAGAA	CTTCTCCCGG	TGCCTGGAGC	TGCAGTGTCA	GCCCCGACTCC	420
TCAACCCTGT	AAGCTT					436

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

## Seq List 10-644355.txt

- (A) LENGTH: 449 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCTGC	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGGTCAGGA	GGTGGATCC				449

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCGGAG	GTGGCACCCA	GGACTGCTCC	TTCCAACACA	GCCCCATCTC	CTCCGACTTC	60
GCTGTCAAAA	TCCGTGAGCT	GTCTGACTAC	CTGCTTCAAG	ATTACCCAGT	CACCGTGGCC	120
TCCAACCTGC	AGGACGAGGA	GCTCTGCGGG	GGCCTCTGGC	GGCTGGTCCT	GGCACAGCGC	180
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG	TCCAAGATGC	AAGGCTTGCT	GGAGCGCGTG	240
AACACGGAGA	TACACTTTGT	CACCAAATGT	GCCTTTCAGC	CCCCCCCCAG	CTGTCTTCGC	300
TTCGTCCAGA	CCAACATCTC	CCGCCTCCTG	CAGGAGACCT	CCGAGCAGCT	GGTGGCGCTG	360
AAGCCCTGGA	TCACTCGCCA	GAACCTCTCC	CGGTGCCTGG	AGCTGCAGTG	TCAGCCCCGAC	420
TCCTCAACCC	TGTAAGCTT					439

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCTGC	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGGTCAGGA	GGTGGGTCAG	GAGGTGGATC	C		461

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGATCCGGAG	GTGGCTCAGG	GGGAGGTAGT	GGTACCCAGG	ACTGCTCCTT	CCAACACAGC	60
CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	120
TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	180
CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	240
GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	CACCTTTGTCA	CCAAATGTGC	CTTTCAGCCC	300
CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	360
GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	ACTCGCCAGA	ACTTCTCCCC	GTGCCTGGAG	420
CTGCAGTGTC	AGCCCCACTC	CTCAACCCTG	TAAGCTT			457

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GATCCGGAGG	TACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	360
GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	GACTACCTGC	TTCAAGATTA	CCCAGTCACC	420
GTGGCCTCCA	ACCTGCAG					438

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GATCCGGAGG	TGGCACCCAG	GACTGCTCCT	TCCAACACAG	CCCCATCTCC	360
TCCGACTTCG	CTGTCAAAAT	CCGTGAGCTG	TCTGACTACC	TGCTTCAAGA	TTACCCAGTC	420
ACCGTGGCCT	CCAACCTGCA	G				441

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GGTCAGGAGG	TGGATCCGGA	GGTACCCAGG	ACTGCTCCTT	CCAACACAGC	360
CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	420
TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG				450

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GATCCGGAGG	TGGCTCAGGG	GGAGGTAGTG	GTACCCAGGA	CTGCTCCTTC	360
CAACACAGCC	CCATCTCCTC	CGACTTCGCT	GTCAAAATCC	GTGAGCTGTC	TGACTACCTG	420
CTTCAAGATT	ACCCAGTCAC	CGTGGCCTCC	AACCTGCAG			459

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCGTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GGTCAGGAGG	TGGGTCAGGA	GGTGGATCCG	GAGGTGGCAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
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CGGCTCAAGA	CTGTGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGCCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GGTCAGGAGG	TGGGTCAGGA	GGTGGATCCG	GAGGTGGCTC	AGGGGGAGGT	360
AGTGGTACCC	AGGACTGCTC	CTTCCAACAC	AGCCCCATCT	CCTCCGACTT	CGCTGTCAAA	420
ATCCGTGAGC	TGTCTGACTA	CCTGCTTCAA	GATTACCCAG	TCACCGTGGC	CTCCAACCTG	480
CAG						483

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCCGATTACC	CAGTCACCGT	GGCCTCCAAC	CTGCAGGACG	AGGAGCTCTG	CGGGGGCCTC	60
TGGCGGCTGG	TCCTGGCACA	GCGCTGGATG	GAGCGGTCA	AGACTGTCGC	TGGGTCCAAG	120
ATGCAAGGTG	TGCTGGAGCG	CGTGAACACG	GAGATACACT	TTGTCACCAA	ATGTGCCTTT	180
CAGCCCCCCC	CCAGCTGTCT	TCGCTTCGTC	CAGACCAACA	TCTCCCGCCT	CCTGCAGGAG	240
ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	300
CTGGAGCTGC	AGTGTGAGCC	CGACTCCTCA	ACCCTGGGCG	GTGGGTGAGG	AGGTGGGTCA	360
GGAGGTGGAT	CCGGAGGTGG	CACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	420
GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	GACTACCTGC	TTCAA		465

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCCGCCTCCA	ACCTGCAGGA	CGAGGAGCTC	TGCGGGGGCC	TCTGGCGGCT	GGTCCTGGCA	60
CAGCGCTGGA	TGGAGCGGCT	CAAGACTGTC	GCTGGGTCCA	AGATGCAAGG	CTTGCTGGAG	120
CGCGTGAACA	CGGAGATACA	CTTTGTCACC	AAATGTGCCT	TTCAGCCCCC	CCCCAGCTGT	180
CTTCGCTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCCGA	GCAGCTGGTG	240
GCGCTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGGT	GCCTGGAGCT	GCAGTGTCAG	300
CCCGACTCCT	CAACCCTGGG	CGGTGGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	360
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	420
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTG		465

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCCGTCGCTG	GGTCCAAGAT	GCAAGGCTTG	CTGGAGCGCG	TGAACACGGA	GATACACTTT	60
GTCACCAAAT	GTGCCTTTCA	GCCCCCCCCC	AGCTGTCTTC	GCTTCGTCCA	GACCAACATC	120
TCCCGCCTCC	TGCAGGAGAC	CTCCGAGCAG	CTGGTGGCGC	TGAAGCCCTG	GATCACTCGC	180

## Seq List 10-644355.txt

CAGAACTTCT	CCCCGGTGCCT	GGAGCTGCAG	TGTCAGCCCC	ACTCCTCAAC	CCTGGGCGGT	240
GGGTCAGGAG	GTGGGTCAGG	AGGTGGATCC	GGAGGTGGCA	CCCAGGACTG	CTCCTTCCAA	300
CACAGCCCCA	TCTCCTCCGA	CTTCGCTGTC	AAAATCCGTG	AGCTGTCTGA	CTACCTGCTT	360
CAAGATTACC	ACTTCACCGT	GGCCTCCAAC	CTGCAGGACG	AGGAGCTCTG	CGGGGGCCTC	420
TGGCGGCTGG	TCCTGGCACA	GCGCTGGATG	GAGCGGCTCA	AGACT		465

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCG	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGGGCGG	TGGGTCAGGA	240
GGTGGGTCCG	GAGGTGGATC	CGGAGGTGGC	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTCT	CTGGG		465

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCCA	CTCCTCAACC	CTGGGCGGTG	GGTCAGGAGG	TGGGTCAGGA	180
GGTGGATCCG	GAGGTGGCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	360
CGCTGGATGG	AGCGGCTCAA	GACTGTCTGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	420
GTGAACACGG	AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCC		465

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCCCCGTTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCCGA	GCAGCTGGTG	60
GCGCTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGGT	GCCTGGAGCT	GCAGTGTGAG	120
CCCGACTCCT	CAACCCTGGG	CGGTGGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	180
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	240
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	300
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	360

## Seq List 10-644355.txt

CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 420  
 CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCAGCT GTCTT 465

## (2) INFORMATION FOR SEQ ID NO:142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCCACCAACA	TCTCCCGCCT	CCTGCAGGAG	ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	60
TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	CTGGAGCTGC	AGTGTGAGCC	CGACTCCTCA	120
ACCCTGGGCG	GTGGGTGAGG	AGGTGGGTCA	GGAGGTGGAT	CCGGAGGTGG	CACCCAGGAC	180
TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	240
GACTACCTGC	TTCAAGATTA	CCCAGTCACC	GTGGCCTCCA	ACCTGCAGGA	CGAGGAGCTC	300
TGCGGGGGCC	TCTGGCGGCT	GGTCCTGGCA	CAGCGCTGGA	TGGAGCGGCT	CAAGACTGTC	360
GCTGGGTCCA	AGATGCAAGG	CTTGCTGGAG	CGCGTGAACA	CGGAGATACA	CTTTGTCACC	420
AAATGTGCCT	TTCAGCCCCC	CCCCAGCTGT	CTTCGCTTCG	TCCAG		465

## (2) INFORMATION FOR SEQ ID NO:143:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	1	5	10	15
Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	20	25	30	
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	35	40	45	
Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	50	55	60	
Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	65	70	75	80
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	85	90	95	
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	100	105	110	
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	115	120	125	
Glu	Leu	Gln	Cys	Gln	Pro											130			

## (2) INFORMATION FOR SEQ ID NO:144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Thr  Gln Asp Cys  Ser Phe Gln His Ser  Pro Ile Ser Ser Asp Phe Ala
 1      5      10      15
Val  Lys Ile Arg  Glu Leu Ser Asp Tyr  Leu Leu Gln Asp Tyr Pro Val
      20      25      30
Thr  Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp
      35      40      45
Arg  Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala
      50      55      60
Gly  Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
65      70      75      80
Phe  Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
      85      90      95
Val  Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
      100      105      110
Val  Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
      115      120      125
Glu  Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
      130      135

```

## (2) INFORMATION FOR SEQ ID NO:145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

Thr  Gln Asp Cys  Ser Phe Gln His Ser  Pro Ile Ser Ser Asp Phe Ala
 1      5      10      15
Val  Lys Ile Arg  Glu Leu Ser Asp Tyr  Leu Leu Gln Asp Tyr Pro Val
      20      25      30
Thr  Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp
      35      40      45
Arg  Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala
      50      55      60
Gly  Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
65      70      75      80
Phe  Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
      85      90      95
Val  Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
      100      105      110
Val  Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
      115      120      125
Glu  Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser
      130      135      140
Pro  Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu
145      150      155      160
Leu  Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala
      165      170      175
Trp  Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly
      180      185      190
Glu  Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Val Glu
      195      200      205
His

```



## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTACCA	AATGTGCCTT	TCAGCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTGAGC	CC		402

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTACCA	AATGTGCCTT	TCAGCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTGAGC	CCGACTCCTC	AACCCTGCCA	420
CCCCCATGGA	GTCCCCGGCC	CCTGGAGGCC	ACAGCCCCGA	CAGCCCCGCA	GCCCCCTCTG	480
CTCCTCCTAC	TGCTGCTGCC	CGTGGGCCTC	CTGCTGCTGG	CCGCTGCCTG	GTGCCTGCAC	540
TGGCAGAGGA	CGCGGCGGAG	GACACCCCGC	CCTGGGGAGC	AGGTGCCCCC	CGTCCCCAGT	600
CCCCAGGACC	TGCTGCTTGT	GGAGCACTGA				630

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

gly	gly	gly	ser	gly	gly	gly	ser	gly	gly	gly	ser	gly	gly	gly	ser
1				5				10					15		
gly	gly	gly	ser	gly	gly	gly	ser	gly	gly	gly	ser	gly			
			20					25							

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala Pro Thr Ala  
1 5 10 15  
Gly Gln Pro Pro Leu  
20

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala Pro Thr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Val Glu Thr Val Phe His Arg Val Ser Gln Asp Gly Leu Leu Thr Ser  
1 5 10 15